

SEQUENCE LISTING

<110> Meyers, Rachel A.
MacBeth, Kyle J.

<120> 14094, A NOVEL TRYPSIN FAMILY MEMBER AND
USES THEREFOR

<130> 10448-046002

<150> US 09/633,300
<151> 2000-08-08

<150> US 60/200,621
<151> 2000-04-28

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2948
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (628)...(1986)

<221> misc_feature
<222> (1)...(2948)
<223> n = A,T,C or G

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gtatcccttc cagggtaaaaa agcaaaaagaa ttccgggttt ctgtatcctt ttcacttact 180
gttaccctact ttgcctcgtc ttccaccctgt ccaaacacccg gtctccaatt tgcccttcag 240
agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca 300
ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atataacttcc 360
caaactccaa aaaaaaaaccg gaattcagcc tggtaagtc caagctgaat tccgggtggg 420
ggaaggaccg ggcacccggac ggctcgggta ctttcgttct taatttaggtc atgcccgtat 480
gagccaggaa agggctgtgt ttatggaaag ccagtaaacac tggccctac tatctttcc 540
gtgggtgccat ctacattttt gggactcggg aattatgagg tagaggtgga ggcggagccg 600
gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt 654
Met Gly Glu Asn Asp Pro Pro Ala Val

1

5

gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa 702
Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
10 15 20 25

ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg 750
Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
30 35 40

tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile 45 50 55	798
gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys 60 65 70	846
tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile 75 80 85	894
gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr 90 95 100 105	942
cgc tgt gtc cgg gtg ggt cag aat gcc gtg ctc cag gtg ttc aca Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr 110 115 120	990
gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr 125 130 135	1038
gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser 140 145 150	1086
gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe 155 160 165	1134
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His 170 175 180 185	1182
cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr 190 195 200	1230
ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile 205 210 215	1278
gtg ggt gga aac atg tcc ctc tcg cag tgg ccc tgg cag gcc agc Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser 220 225 230	1326
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Ser Val Ile Thr Pro 235 240 245	1374
ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro 250 255 260 265	1422
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca	1470

Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro				
270	275	280		
gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag				1518
Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys				
285	290	295		
cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca				1566
Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro				
300	305	310		
ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa				1614
Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu				
315	320	325		
gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc				1662
Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala				
330	335	340	345	
aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc				1710
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val				
350	355	360		
cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc				1758
Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly				
365	370	375		
atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg				1806
Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val				
380	385	390		
gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg				1854
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg				
395	400	405		
agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca				1902
Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala				
410	415	420	425	
gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac				1950
Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp				
430	435	440		
tgg atc cac gag cag atg gag aga gac cta aaa acc tgaaaaggaa				1996
Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr				
445	450			
ggggacaagt agccacctga gttcctgagg tcatgaagac agcccgatcc tccccctggac				2056
tccctgttag gaacctgcac acgagcagac acccttggag ctctgagttc cggcaccagt				2116
agcaggcccg aaagaggcac cttccatct gattccagca caaccttcaa gtcgttttt				2176
gtttttgtt tttttagat ggagtctcgc tctgttgcgg agctggagt gcagtggcga				2236
aatccctgtct cactgcagcc tccgcttccc tggttcaagc gattctcttg cctcagcttc				2296
cccagtagct gggaccacag gtgcccggca ccacacccaa ctaatttttg tatttttagt				2356
agagacaggg tttcaccatg ttggccaggc tgctctcaaa cccctgaccc caaatgatgt				2416
gcctgcttca gcctccacaca gtgctggat tacaggcatg ggccaccacg cctaggctca				2476
cgctcccttc tgatcttac taagaacaaa agaagcagca acttgcaagg gcgcccttcc				2536
ccactggtcc atctggttt ctctccaggg gtcttgcaaa attcctgacg agataagcag				2596

ttatgtgacc tcacgtgcaa agccaccaac agccactcgaaaagacgca ccagccaga	2656
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<210> 2
<211> 453
<212> PRT
<213> Homo sapiens

<400> 2	
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1 5 10 15	
Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp	
20 25 30	
Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe	
35 40 45	
Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala	
50 55 60	
Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg	
65 70 75 80	
Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser	
85 90 95	
Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly	
100 105 110	
Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met	
115 120 125	
Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln	
130 135 140	
Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser	
145 150 155 160	
Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu	
165 170 175	
Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu	
180 185 190	
Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly	
195 200 205	
His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu	
210 215 220	
Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His	
225 230 235 240	
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala	
245 250 255	
His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val	
260 265 270	
Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu	
275 280 285	
Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp	
290 295 300	
Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile	
305 310 315 320	
Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys	
325 330 335	
Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala	
340 345 350	

Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys Ile
 355 360 365
 Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu
 370 375 380
 Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
 385 390 395 400
 Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly
 405 410 415
 Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val
 420 425 430
 Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu
 435 440 445
 Arg Asp Leu Lys Thr
 450

<210> 3
 <211> 1362
 <212> DNA
 <213> Homo sapiens

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 ctgtcactgc tgccattgaa gtttttcca atcatgtca ttgggatcat tgcattgata 180
 ttagcactgg ccattggctc gggcatccac ttgcactgct cagggaaagta cagatgtcgc 240
 tcatcctta agtgtatcga gctgatagct cgatgtgacg gagtctcgga ttgcaaagac 300
 ggggaggacg agtaccgctg tgcgggggtg ggtggtcaga atgcccgtct ccaggtgttc 360
 acagctgctt cgtggaaagac catgtgctcc gatgactgga agggtaacta cgcaaatgtt 420
 gcctgtgccc aactgggtt cccaaagctat gtgagtcag ataacctcag agtgagctcg 480
 ctggaggggc agttccggga ggagtttgtc tccatcgatc acctttggcc agatgacaag 540
 gtgactgcat tacaccactc agtatatgtg agggaggat gtgcctctgg ccacgtggtt 600
 accttgcagt gcacagccctg tggcataga aggggttaca gctcacgcat cgtgggtgga 660
 aacatgtctc tgccttcgcgtt gtcggccctgg caggccagcc ttcaatccca gggctaccac 720
 ctgtgcgggg gctctgtcat cacccccctg tggatcatca ctgctgcaca ctgtgtttat 780
 gacttgtacc tccccaaatc atggaccatc caggtgggtc tagttccct gttggacaat 840
 ccagccccat cccacttgggt ggagaagatt gtctaccaca gcaagtacaa gccaaagagg 900
 ctgggcaatg acatcgccct tatgaagctg gccggccac tcacgttcaa taaaatgtatc 960
 cagccctgtgt gcctgccccaa ctgtgaagag aactcccccg atggaaaagt gtgctggacg 1020
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 gtcctttgtt gttccaaacaa gatctgcac cacaggacg tgcacgggtt catcatctcc 1140
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 gggggggccccc tgggtgttca agagaggagg ctgtggaaat tagtggggac gaccagctt 1260
 ggcacatggcgt ggcacagatc gaaacaaggct ggggtgtaca cccgtgtcac ctccttcctg 1320
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<210> 4
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 4
 Ile Val Gly Gly Arg Glu Ala Gln Pro Gly Ser Phe Gly Ser Pro Trp
 1 5 10 15
 Gln Val Ser Leu Gln Val Arg Ser Gly Gly Ser Arg Lys His Phe

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Cys Gly Gly Ser Leu Ile Ser Glu Asn Trp Val Leu Thr Ala Ala His			
35	40	45	
Cys Val Ser Gly Ala Ala Ser Ala Pro Ala Ser Ser Val Arg Val Ser			
50	55	60	
Leu Ser Arg Val Arg Leu Gly Glu His Asn Leu Ser Leu Thr Glu Gly			
65	70	75	80
Thr Glu Gln Lys Phe Asp Val Lys Lys Thr Ile Ile Val His Pro Asn			
85	90	95	
Tyr Asn Pro Asp Thr Leu Asp Asn Gly Ala Tyr Asp Asn Asp Ile Ala			
100	105	110	
Leu Leu Lys Leu Lys Ser Pro Gly Val Thr Leu Gly Asp Thr Val Arg			
115	120	125	
Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp Leu Pro Val Gly Thr Thr			
130	135	140	
Cys Thr Val Ser Gly Trp Gly Arg Arg Pro Thr Lys Asn Leu Gly Leu			
145	150	155	160
Ser Asp Thr Leu Gln Glu Val Val Val Pro Val Val Ser Arg Glu Thr			
165	170	175	
Cys Arg Ser Ala Tyr Glu Tyr Gly Gly Thr Asp Asp Lys Val Glu Phe			
180	185	190	
Val Thr Asp Asn Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala			
195	200	205	
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Asn Arg			
210	215	220	
Asp Gly Arg Trp Glu Leu Val Gly Ile Val Ser Trp Gly Ser Tyr Gly			
225	230	235	240
Cys Ala Arg Gly Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr			
245	250	255	
Leu Asp Trp Ile			
260			

<210> 5
 <211> 226
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 5
 Arg Ile Val Gly Gly Ser Glu Ala Lys Ile Gly Ser Phe Pro Trp Gln
 1 5 10 15
 Val Ser Leu Gln Cys Gly Gly Ser Leu Ile Ser Pro Arg Trp Val Leu
 20 25 30
 Thr Ala Ala His Cys Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
 35 40 45
 Gly Glu Glu Thr Glu Gly Gly Pro Arg Leu Asp Ser Pro Gly Gly Gln
 50 55 60
 Val Ile Lys Val Ser Lys Ile Ile Glu Val His Pro Asn Tyr Asn Asn
 65 70 75 80
 Asp Ile Ala Leu Leu Lys Leu Lys Glu Pro Val Thr Leu Ser Asp Ser
 85 90 95
 Asn Thr Val Arg Pro Ile Cys Leu Pro Ser Ser Asn Glu Ile Lys Thr
 100 105 110
 Ser Glu Gly Asn Thr Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
 115 120 125

Trp Gly Arg Thr Ser Glu Gly Pro Glu Glu Ser Gly Gly Gly Ser Leu
 130 135 140
 Pro Asp Val Leu Gln Glu Val Asn Val Pro Ile Val Ser Asn Glu Thr
 145 150 155 160
 Cys Arg Met Leu Cys Ala Gly Tyr Leu Glu Gly Gly Asn Thr Pro Gly
 165 170 175
 Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Val
 180 185 190
 Leu Val Gly Ile Val Ser Trp Gly Ser Ser Ser Leu Tyr Gly Cys Ala
 195 200 205
 Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr Leu Asp
 210 215 220
 Trp Ile
 225

<210> 6
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 6
 Ser Thr Cys Gly Gly Pro Asp Glu Phe Gln Cys Gly Ser Gly Arg Arg
 1 5 10 15
 Cys Ile Pro Arg Ser Trp Val Cys Asp Gly Asp Pro Asp Cys Glu Asp
 20 25 30
 Gly Ser Asp Glu Ser Leu Glu Asn Cys Ala Ala
 35 40

<210> 7
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 7
 Val Gly Gly Ser Ser Arg Cys Glu Gly Arg Val Glu Val Arg His Asp
 1 5 10 15
 Gly Ser Lys Trp Gly Thr Val Cys Asp Ser Ser Trp Ser Leu Arg Asp
 20 25 30
 Ala Asn Val Asp Pro Gln Ala Ser Lys Val Cys Arg Gln Leu Gly Cys
 35 40 45
 Gly Gly Ala Val Ser Leu Leu Gly Pro Tyr Phe Ser Glu Gly Gly
 50 55 60
 Pro Ala Gly Gln Arg Glu Ile Trp Leu Asp Gly Val Asn Cys Ser Gly
 65 70 75 80
 Asn Glu Thr Ser Leu Ser Gln Cys Pro Val Arg Val Thr Pro Pro Gly
 85 90 95
 Leu Ser Arg Gln Cys Ser His Asp Gly Glu Asp Ala Gly Val Val Cys
 100 105 110
 Ser

<210> 8
<211> 5
<212> PRT
<213> Homo sapiens

<400> 8
Arg Ile Val Gly Gly
1 5

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<221> VARIANT
<222> 2
<223> Xaa = Asp or Glu

<221> VARIANT
<222> 5
<223> Xaa = Gly or Ser

<400> 9
Gly Xaa Ser Gly Xaa
1 5

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<221> VARIANT
<222> 1
<223> Xaa = Leu, Ile, Val, or Met

<221> VARIANT
<222> 2
<223> Xaa = Ser or Thr

<221> VARIANT
<222> 4
<223> Xaa = Ser, Thr, Ala, or Gly

<400> 10
Xaa Xaa Ala Xaa His Cys
1 5

<210> 11
<211> 2951
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> (628) ... (1989)

<221> misc_feature
 <222> (1) ... (2951)
 <223> n = A, T, C or G

<400> 11

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 gtttgcataaa tccagttttc ttgtaaagat tggggggtaa ataacagagg tggcttatga 60
 gtatTTCTTC cagggtaaaa agcaaaagaa ttccggTTT ctgtatcCTT ttcacttaCT
 gttaccact ttgcctcgTC ttccaccCTGT ccaaacacCC gtctccaATT tgccCTTCAG 120
 agaacttaAG tcaaggagAG ttgaaATTCA caggCCAGGG cacatCTTT atttATTTCA 180
 ttatgttGGC caacagaACT tgattgtAAA taataataAA gaaatCTGTT atataCTTTC 240
 caaactCCAA aaaaaaACCG gaattcAGCC tggTTAAGTC caagCTGAAT tccgggtGGG 300
 ggaaggACCG ggcACCGGAC ggCTCGGTa cttcgttCT taattAGGTc atGCCCGTAT 360
 gagCCAGGAA agggCTGTGT ttatggAAAG ccAGTAACAC tGTGGCCTAC tatCTCTTC 420
 gtggTCCat ctacatTTT gggactCGGG aattatgAGG tagaggTGGa ggcggAGCCG 480
 gatgtcAGAG gtcctgAAAT agtCACC ATG ggg gAA AAT gAT CCG CCT GCT gTT 540
 gatgtcAGAG gtcctgAAAT agtCACC ATG ggg gAA AAT gAT CCG CCT GCT gTT 600
 Met Gly Glu Asn Asp Pro Pro Ala Val 654

1 5

gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa 702
 Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
 10 15 20 25

ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg 750
 Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
 30 35 40

tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att 798
 Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile
 45 50 55

gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc 846
 Ala Leu Ile Leu Ala Leu Ile Gly Leu Gly Ile His Phe Asp Cys
 60 65 70

tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata 894
 Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile
 75 80 85

gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac 942
 Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 90 95 100 105

cgc tgt gtc cgg gtg ggt cag aat gcc gtg ctc cag gtg ttc aca 990
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr
 110 115 120

gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac 1038
 Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr
 125 130 135

qca aat qtt qcc tqt qcc caa ctg ggt ttc cca agc tat gtg agt tca 1086

Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser			
140	145	150	
gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cg ^g gag gag ttt			1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe			
155	160	165	
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac			1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His			
170	175	180	185
cac tca gta tat gtg agg gag gga t ^g t g ^c c t ^c t g ^g g c ^a c gtg gtt acc			1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr			
190	195	200	
ttg cag tgc aca gcc t ^g t g ^g t cat aga agg ggc tac agc tca cgc atc			1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile			
205	210	215	
gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc			1326
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser			
220	225	230	
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc			1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro			
235	240	245	
ctg tgg atc atc act gct gca cac t ^g t gtt tat gac ttg tac ctc ccc			1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro			
250	255	260	265
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca			1470
Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro			
270	275	280	
gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag			1518
Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys			
285	290	295	
cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca			1566
Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro			
300	305	310	
ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa			1614
Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu			
315	320	325	
gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc			1662
Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala			
330	335	340	345
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Thr Glu Asp Gly Ala Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala			
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Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly			

365

370

375

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Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly																																																																			
380	385	390		gtg gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag	1854	Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu		395	400	405		agg agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc	1902	Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys		410	415	420	425	gca gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg	1950	Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu		430	435	440		gac tgg atc cac gag cag atg gag aga gac cta aaa acc tgaagagggaa	1999	Asp Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr		445	450			ggggacaagt agccacctga gttcctgagg ttagtgaagac agccccatcc tccccctggac	2059	tcccgtaga gAACCTGcac acgagcagac acccttggag ctctgagttc cggcaccagt	2119	agcaggccccg aaagaggcac cttccatct gattccagca caaccttcaa gctgctttt	2179	gtttttgtt tttttgagat ggagtctcg tctgttgcggc aggctggagt gcagtgccgaa	2239	aatccctgct cactgcagcc tccgcttccc tggttcaagc gattctcttg cctcagcttc	2299	cccagtagct gggaccacag gtgcccggca ccacacccaa ctaattttg tatttttagt	2359	agagacagggtt ttcaccatg ttggccaggc tgctctcaaa cccctgacccaa caaatgtatgt	2419	gcctgcttca gcctccaca gtgctggat tacaggcatg ggccaccacg cctagcctca	2479	cgctccttcc ttagtcttcc taagaacaaa agaagcagca acttgcaagg gcggccttcc	2539	ccactggtcc atctgggttt ctctccagggtt gtcttgcggc attcctgaccc agataagcag	2599	ttatgtgacc tcacgtgcaaa agccaccaac agccactcgaaa aaaaagacgca ccagccaga	2659	agtgcagaac tgcaactgcact gcacgttttcc atctcttaggg accagaacca aacccaccc	2719	ttctacttcc aagacttattttt ttcacatgtg gggagggtttaa tcttaggaatg actcggtttaa	2779	ggcctatttt catgatttct ttgttagcatt tgggtgttgc cgtattatttgc tccttgatt	2839	ccaaataata tggttcccttc cctcatwraa maaaaaaaaaaaaaaaarr rmrrssgcta	2899	vavmarktta gagaaaaaaac ctacccacrc cttccccctg aamctraaam ya	2951
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